

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:22:06 ; Search time 88.16 Seconds

(Without alignments)
38.555 Million cell updates/sec

Title: US-09-331-631A-33

Perfect score: 77

Sequence: 1 CXXCXXCXXXXXXXXXXCXXCXXCXXC 29

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	43	5	09VDN2
2	77	100.0	49	5	023947
3	77	100.0	49	5	023948
4	77	100.0	152	5	09XVX3
5	77	100.0	164	5	022048
6	77	100.0	188	5	018238
7	77	100.0	273	5	020000
8	77	100.0	314	5	023190
9	77	100.0	325	2	083828
10	77	100.0	625	10	09SP15
11	77	100.0	666	10	09SP14
12	77	100.0	666	10	09SP14
13	68	88.3	39	13	09PVG7
14	68	88.3	46	4	016861
15	68	88.3	62	10	065918
16	68	88.3	72	5	09VI99
17	68	88.3	73	10	041615
18	68	88.3	74	5	09VIAI
19	68	88.3	75	5	096388

20	68	88.3	80	10	09SG42	09SG42 arabidopsis
21	68	88.3	83	11	09JM45	09JM45 mus muscu
22	68	88.3	84	13	090248	090248 bombyx bom
23	68	88.3	87	10	080641	080641 arabidopsis
24	68	88.3	89	11	088459	088459 mus muscu
25	68	88.3	91	10	049134	049134 fragaria an
26	68	88.3	97	10	038939	038939 arabidopsis
27	68	88.3	101	10	065313	065313 lavatera th
28	68	88.3	101	10	09XG33	09XG33 gerbera hyb
29	68	88.3	102	10	024040	024040 lavatera th
30	68	88.3	103	10	080848	080848 arabidopsis
31	68	88.3	106	10	049593	049593 arabidopsis
32	68	88.3	108	10	082328	082328 arabidopsis
33	68	88.3	110	6	09XSV4	09XSV4 canis fami
34	68	88.3	110	10	065066	065066 picea maria
35	68	88.3	112	10	043615	043615 petunia hyb
36	68	88.3	121	13	091450	091450 salvelinus
37	68	88.3	129	10	09LR14	09LR14 arabidopsis
38	68	88.3	136	2	09X8F4	09X8F4 streptomyce
39	68	88.3	169	4	014564	014564 homo sapien
40	68	88.3	177	10	09LIU5	09LIU5 oryza sativ
41	68	88.3	178	13	09IAR5	09IAR5 fuqua rubrip
42	68	88.3	191	6	028583	028583 ovis aries
43	68	88.3	191	6	09NOL8	09NOL8 macropus eu
44	68	88.3	230	11	064507	064507 mus muscu
45	68	88.3	242	5	019919	019919 caenorhabdi

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	43 AA.
09VDN2	09VDN2	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DE	DE	01-JUN-2000 (TREMBLrel. 14, Last annotation update)		
GN	GN	CG5097 PROTEIN.		
OS	OS	Drosophila melanogaster (Fruit fly).		
OC	OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OX	OX	Ephydroidae; Drosophilidae; Drosophila.		
RN	RN	NCBI_TaxID=7227;		
RP	RP	SEQUENCE FROM N.A.		
RC	RC	STRAIN=BERKELEY;		
RX	RX	MEDLINE=20196006; PubMed=10731132;		
RA	RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,		
RA	RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	RA	Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,		
RA	RA	Brandon R.C., Rogers Y.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,		
RA	RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,		
RA	RA	Abriil J.F., Adayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,		
RA	RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,		
RA	RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,		
RA	RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,		
RA	RA	Burky K.C., Busam D.A., Butler H., Cadlen E., Center A., Chandra I.,		
RA	RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,		
RA	RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,		
RA	RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		
RA	RA	Dubin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,		
RA	RA	Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,		
RA	RA	Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,		
RA	RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,		
RA	RA	Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,		
RA	RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,		
RA	RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,		
RA	RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,		
RA	RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,		
RA	RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,		

RA Mount S.S., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclel J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheller F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Sprydas R., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.W., Weissensbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C. ;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003730; AAF55758.1; -
DR FlyBase; FBgn0038790; CG5097.
DR INTERPRO: IPR000561; -
DR INTERPRO: IPR000966; -
DR PFAM: PF02067; Metallochio_5; 1.
DR PRINTS: PR00872; MTDIPTERA.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
SQ SEQUENCE 43 AA, 4557 MW, E54E722B14E89DFE CRC64;

Query Match	100.0%;	Score 77;	DB 5;	Length 43;
Best Local Similarity	20.7%;	Pred. No. 6.6;		
Matches	6;	Conservative 23;	Mismatches 0;	Indels 0;
			Gaps	0;

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Oy      1  CXXCXXCXXXXXXXXXXCXXCXXC  29
          |:::|:::|:::|:::|:::|
Db      3  CKGCGTNCQDPTKCGDNCACGNQDCKVC  31

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RESULT	2			
ID	023947	PRELIMINARY;	PRT;	49 AA.
AC	023947:			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	TESTIS-SPECIFIC RNA.			
GN	DHTC3.			
OS	Drosophila hydei (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephyridiidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7224;			
	[1]			
RP	SEQUENCE FROM N.A.			
RA	Kuech A., Buenemann H.;			
RL	Submitted (DEC-1990) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: X58114; CAAL117.1; -.			
DR	FLYBASE: FBgn0015096; Dhvd\Mst8.Fa.			
DR	INTERPRO: IPR001450; -.			
DR	PROSITE: PS00198; 4FEAS_FERREDOXIN; UNKNOWN_1.			
Q	SEQUENCE 49 AA; 4610 MW; BE158EC51369F01 CRC64;			

Query Match	100.0%;	Score 77;	DB 5;	Length 49;
Best Local Similarity	20.7%;	Pred. No. 7.1;		
Matches	6;	Conservative	23;	Mismatches 0;
			Indels	0;
			Gaps	0;

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QY      1 CXXCXXCXXXXXXXXXXCXXCXXC 29
         |:|::|:::|:::|:::|:::|
Db      3 CGPCGGCCGPGCCGCPYSCGPGYSC 31

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RESULT	3	
Q23948		
ID	Q23948	PRELIMINARY;
AC	Q23948;	PRT;
DT	01-NOV-1996 (TREMBlrel, 01, Last sequence update)	49 AA.

DT 01-OCT-2000 (TREMBLREL. 15, last annotation update)
DE TESTIS-SPECIFIC RNA.
GN DHTC2.
OS Drosophila hydei (Fruit Fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7224;
RN [1]
RP
RP SEQUENCE FROM N.A.
RA Kuech A., Buenemann H.,
RL Submitted (DEC-1990) to the EMBL/GenBank/DBJ databases.
DR EMBL; X58114; CA41118.1; -
DR FLXBASE; FBgn0015097; Dhyd\ms87fb.
DR INTERPRO; IPR001450; -
DR PROSITE; PS00198; 4PEAS.FERRDOXIN; UNKNOWN_1.
SO SEQUENCE 49 AA; 4550 MW; 24758fbc51369f1d CRC64;

Query Match	100.0%	Score 77;	DB 5;	Length 49;
Best Local Similarity	20.7%	Pred. NO. 7.1;		
Matches	6;	Conservative 23;	Mismatches 0;	Indels 0;
Gaps				0;

```

Qy      1 CXXCXXCXXXXXXCXXCXXCXXC 29
          |:::|:::|:::|:::|:::|
Db      3 CGPCGCGCGCGCCGPCYSCGPCYSC 31

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RESULT	4			
09XVX3				
ID	09XVX3	PRELIMINARY:	PRT:	152 AA.
AC	09XVX3			
DT	01-NOV-1999 (TrEMBLrel. 12, Created)			
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last annotation update)			
DE	C06A1.6. PROTEIN.			
GN	C06A1.6.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea			
OC	Rhabditidae; Pelodierinae; Caenorhabditis.			
OX	NCBI_TaxId=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=94150718; PubMed=7906398;			
RA	McMurray A.;			
RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.			
RT	elegans.";			
SL	Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.			

RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906399;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Dublin R., Favella A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw P., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurtry A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Ritten K., Roopra A., Saunders D., Shownkeen R.,
RA Smalton N., Smith A., Sonhammer E., Staden R., Sutston J.,
RA Thierley-Hieg J., Thomas K., Vaudin M., Vaughan K., Waterson R.,
RA Watson A., Weinstein L., Wilkinson-Sproat J., Wohlman P.;
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RL Nature 368:32-38(1994).
 DR EMBL; Z49886; CAA90055.1; -.
 DR INTERPRO: IPR000561; -.
 DR INTERPRO: IPR001007; -.
 DR INTERPRO: IPR001450; -.
 DR INTERPRO: IPR001502; -.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS00198; 4FETs_FERREDOXIN; UNKNOWN_1.
 DR PROSITE: PS00764; ENDONUCLEASE_TII1; 1.
 DR PROSITE: PS01208; WFC; UNKNOWN_1.

Query Match 88.3%; Score 68; DB 4; Length 46;
Best Local Similarity 17.9%; Pred. No. 40;
Matches 5; Conservative 23; Mismatches 0; Indels 0; Gaps 0;

QY 2 XXXXXXXXXXXXXXXXXXXX 29
DB 9 SRCRCRCRCRCRCRCRCRCRCRCRC 36

RESULT 15

ID 065918 PRELIMINARY; PRT: 62 AA.
AC 065918;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DE 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE GASAS-LIKE PROTEIN (FRAGMENT).
GN SB35.
OS Picea mariana (Black spruce).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3335;
RN [1]
RP SEQUENCE FROM N.A.
RA Perry D.J.; Bousquet J.;
RL Genetics 0:0-0(1998).
DR EMBL; AF051754; AAC32171.1; -.
DR EMBL; AF051753; AAC32170.1; -.
DR MENDEL; 29301; Picma; 1249; 29301.
FT NON_TER 1
SQ SEQUENCE 62 AA; 6886 MW; A576222C14631F35 CRC64;

Query Match 88.3%; Score 68; DB 10; Length 62;
Best Local Similarity 17.9%; Pred. No. 47;
Matches 5; Conservative 23; Mismatches 0; Indels 0; Gaps 0;

QY 2 XXXXXXXXXXXXXXXXXXXX 29
DB 2 SECGRCSYRCSATSHKPCMFQCKC 29

Search completed: March 1, 2001, 16:22:07
Job time: 284 sec